

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DellaPenna, Dean
Shintani, David K.
- (ii) TITLE OF INVENTION: TRANSGENIC PLANTS WITH TOCOPHEROL
METHYLTRANSFERASE
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Quarles & Brady
 - (B) STREET: 1 South Pinckney Street
 - (C) CITY: Madison
 - (D) STATE: WI
 - (E) COUNTRY: US
 - (F) ZIP: 53701-2113
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Seay, Nicholas J.
 - (B) REGISTRATION NUMBER: 27386
 - (C) REFERENCE/DOCKET NUMBER: 920905.90024
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 608-251-5000
 - (B) TELEFAX: 608-251-9166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 954 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..954
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG Met 1	GTT Val	TAC Tyr	CAT His	GTT Val 5	AGG Arg	CCT Pro	AAG Lys	CAC His	GCC Ala 10	CTG Leu	TTC Phe	TTA Leu	GCA Ala	TTC Phe 15	TAT Tyr	48
TGT Cys	TAT Tyr	TTC Phe	TCT Ser 20	TTG Leu	CTT Leu	ACC Thr	ATG Met	GCC Ala 25	AGC Ser	GCC Ala	ACC Thr	ATT Ile	GCC Ala 30	AGT Ser	GCA Ala	96
GAC Asp	CTC Leu	TAC Tyr 35	GAA Glu	AAA Lys	ATT Ile	AAA Lys	AAT Asn 40	TTC Phe	TAC Tyr	GAC Asp	GAC Asp	TCC Ser 45	AGC Ser	GGT Gly	CTC Leu	144
TGG Trp 50	GAA Glu	GAC Asp	GTT Val	TGG Trp	GGT Gly	GAG Glu 55	CAT His	ATG Met	CAC His	CAC His	GGC Gly 60	TAC Tyr	TAC Tyr	GGT Gly	CCC Pro	192
CAC His 65	GGC Gly	ACC Thr	TAT Tyr	CGG Arg	ATC Ile 70	GAT Asp	CGC Arg	CGC Arg	CAG Gln	GCT Ala 75	CAA Gln	ATT Ile	GAT Asp	CTG Leu 80	ATC Ile	240
AAA Lys	GAA Glu	CTA Leu	TTG Leu	GCC Ala 85	TGG Trp	GCA Ala	GTG Val	CCC Pro	CAA Gln 90	AAT Asn	AGC Ser	GCC Ala	AAA Lys	CCA Pro 95	CGA Arg	288
AAA Lys	ATT Ile	CTC Leu	GAT Asp 100	TTA Leu	GGC Gly	TGT Cys	GGC Gly	ATT Ile 105	GGC Gly	GGC Gly	AGT Ser	AGT Ser	TTG Leu 110	TAC Tyr	TTG Leu	336
GCC Ala	CAG Gln	CAA Gln 115	CAC His	CAA Gln	GCA Ala	GAA Glu	GTG Val 120	ATG Met	GGG Gly	GCT Ala	AGT Ser	CTT Leu 125	TCC Ser	CCA Pro	GTG Val	384
CAG Gln 130	GTG Val	GAA Glu	CGG Arg	GCG Ala	GGG Gly	GAA Glu 135	AGG Arg	GCC Ala	AGG Arg	GCC Ala	CTG Leu 140	GGG Gly	TTG Leu	GGC Gly	TCA Ser	432
ACC Thr 145	TGC Cys	CAG Gln	TTT Phe	CAG Gln	GTG Val 150	GCC Ala	AAT Asn	GCC Ala	TTG Leu	GAT Asp 155	TTG Leu	CCC Pro	TTT Phe	GCT Ala	TCC Ser 160	480
GAT Asp	TCC Ser	TTT Phe	GAC Asp 165	TGG Trp	GTT Val	TGG Trp	TCG Ser	TTG Leu	GAA Glu 170	AGT Ser	GGG Gly	GAG Glu	CAC His	ATG Met 175	CCC Pro	528
AAC Asn	AAA Lys	GCT Ala	CAG Gln 180	TTT Phe	TTA Leu	CAA Gln	GAA Glu 185	GCT Ala	TGG Trp	CGG Arg	GTA Val	CTT Leu	AAA Lys 190	CCA Pro	GGT Gly	576
GGC Gly	CGT Arg	CTG Leu 195	ATT Ile	TTA Leu	GCG Ala	ACC Thr	TGG Trp 200	TGT Cys	CAT His	CGT Arg	CCC Pro	ATT Ile 205	GAT Asp	CCC Pro	GGC Gly	624
AAT Asn 210	GGC Gly	CCC Pro	CTG Leu	ACT Thr	GCC Ala	GAT Asp 215	GAA Glu	CGT Arg	CGC Arg	CAT His	CTC Leu 220	CAA Gln	GCC Ala	ATC Ile	TAT Tyr	672
GAC Asp 225	GTT Val	TAC Tyr	TGT Cys	TTG Leu	CCC Pro 230	TAT Tyr	GTG Val	GTT Val	TCC Ser	CTG Leu 235	CCG Pro	GAC Asp	TAC Tyr	GAG Glu	GCG Ala 240	720
ATC Ile	GCC Ala	AGG Arg	GAA Glu	TGT Cys 245	GGG Gly	TTT Phe	GGG Gly	GAA Glu	ATT Ile 250	AAG Lys	ACT Thr	GCC Ala	GAT Asp	TGG Trp 255	TCA Ser	768

GTG GCG GTG GCA CCT TTT TGG GAC CGG GTG ATT GAG TCT GCG TTC GAT	816
Val Ala Val Ala Pro Phe Trp Asp Arg Val Ile Glu Ser Ala Phe Asp	
260 265 270	
CCC CGG GTG TTG TGG GCC TTG GGG CAA GCG GGG CCA AAA ATT ATC AAT	864
Pro Arg Val Leu Trp Ala Leu Gly Gln Ala Gly Pro Lys Ile Ile Asn	
275 280 285	
GCC GCC CTG TGT TTA CGA TTA ATG AAA TGG GGC TAT GAA CGG GGA TTA	912
Ala Ala Leu Cys Leu Arg Leu Met Lys Trp Gly Tyr Glu Arg Gly Leu	
290 295 300	
GTG CGT TTT GGC TTA TTA ACG GGG ATA AAG CCT TTA GTT TGA	954
Val Arg Phe Gly Leu Leu Thr Gly Ile Lys Pro Leu Val *	
305 310 315	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Val Tyr His Val Arg Pro Lys His Ala Leu Phe Leu Ala Phe Tyr	
1 5 10 15	
Cys Tyr Phe Ser Leu Leu Thr Met Ala Ser Ala Thr Ile Ala Ser Ala	
20 25 30	
Asp Leu Tyr Glu Lys Ile Lys Asn Phe Tyr Asp Asp Ser Ser Gly Leu	
35 40 45	
Trp Glu Asp Val Trp Gly Glu His Met His His Gly Tyr Tyr Gly Pro	
50 55 60	
His Gly Thr Tyr Arg Ile Asp Arg Arg Gln Ala Gln Ile Asp Leu Ile	
65 70 75 80	
Lys Glu Leu Leu Ala Trp Ala Val Pro Gln Asn Ser Ala Lys Pro Arg	
85 90 95	
Lys Ile Leu Asp Leu Gly Cys Gly Ile Gly Gly Ser Ser Leu Tyr Leu	
100 105 110	
Ala Gln Gln His Gln Ala Glu Val Met Gly Ala Ser Leu Ser Pro Val	
115 120 125	
Gln Val Glu Arg Ala Gly Glu Arg Ala Arg Ala Leu Gly Leu Gly Ser	
130 135 140	
Thr Cys Gln Phe Gln Val Ala Asn Ala Leu Asp Leu Pro Phe Ala Ser	
145 150 155 160	
Asp Ser Phe Asp Trp Val Trp Ser Leu Glu Ser Gly Glu His Met Pro	
165 170 175	
Asn Lys Ala Gln Phe Leu Gln Glu Ala Trp Arg Val Leu Lys Pro Gly	
180 185 190	

Gly Arg Leu Ile Leu Ala Thr Trp Cys His Arg Pro Ile Asp Pro Gly
 195 200 205
 Asn Gly Pro Leu Thr Ala Asp Glu Arg Arg His Leu Gln Ala Ile Tyr
 210 215 220
 Asp Val Tyr Cys Leu Pro Tyr Val Val Ser Leu Pro Asp Tyr Glu Ala
 225 230 235 240
 Ile Ala Arg Glu Cys Gly Phe Gly Glu Ile Lys Thr Ala Asp Trp Ser
 245 250 255
 Val Ala Val Ala Pro Phe Trp Asp Arg Val Ile Glu Ser Ala Phe Asp
 260 265 270
 Pro Arg Val Leu Trp Ala Leu Gly Gln Ala Gly Pro Lys Ile Ile Asn
 275 280 285
 Ala Ala Leu Cys Leu Arg Leu Met Lys Trp Gly Tyr Glu Arg Gly Leu
 290 295 300
 Val Arg Phe Gly Leu Leu Thr Gly Ile Lys Pro Leu Val *
 305 310 315

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1790 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 207..1253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCTCGCATGT TGTGTGGAAT TGTGAGCGGA TAACAATTTT ACACAGGAAA CAGCTATGAC	60
CATGATTACG CCAAGCTCTA ATACGACTCA CTATAGGGAA AGCTGGTACG CCTGCAGGTA	120
CCGGTCCGGA ATTCCCGGGT CGACCCACGC GTCCGCAAAT AATCCCTGAC TTCGTCACGT	180
TTCTTTGTAT CTCCAACGTC CAATAA ATG AAA GCA ACT CTA GCA GCA CCC TCT	233
Met Lys Ala Thr Leu Ala Ala Pro Ser	320 325
TCT CTC ACA AGC CTC CCT TAT CGA ACC AAC TCT TCT TTC GGC TCA AAG	281
Ser Leu Thr Ser Leu Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys	330 335 340
TCA TCG CTT CTC TTT CGG TCT CCA TCC TCC TCC TCC TCA GTC TCT ATG	329
Ser Ser Leu Leu Phe Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met	345 350 355
ACG ACA ACG CGT GGA AAC GTG GCT GTG GCG GCT GCT GCT ACA TCC ACT	377
Thr Thr Thr Arg Gly Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr	360 365 370 375

GAG	GCG	CTA	AGA	AAA	GGA	ATA	GCG	GAG	TTC	TAC	AAT	GAA	ACT	TCG	GGT	425
Glu	Ala	Leu	Arg	Lys	Gly	Ile	Ala	Glu	Phe	Tyr	Asn	Glu	Thr	Ser	Gly	
				380					385					390		
TTG	TGG	GAA	GAG	ATT	TGG	GGA	GAT	CAT	ATG	CAT	CAT	GGC	TTT	TAT	GAC	473
Leu	Trp	Glu	Glu	Ile	Trp	Gly	Asp	His	Met	His	His	Gly	Phe	Tyr	Asp	
				395				400					405			
CCT	GAT	TCT	TCT	GTT	CAA	CTT	TCT	GAT	TCT	GGT	CAC	AAG	GAA	GCT	CAG	521
Pro	Asp	Ser	Ser	Val	Gln	Leu	Ser	Asp	Ser	Gly	His	Lys	Glu	Ala	Gln	
		410					415					420				
ATC	CGT	ATG	ATT	GAA	GAG	TCT	CTC	CGT	TTC	GCC	GGT	GTT	ACT	GAT	GAA	569
Ile	Arg	Met	Ile	Glu	Glu	Ser	Leu	Arg	Phe	Ala	Gly	Val	Thr	Asp	Glu	
	425					430				435						
GAG	GAG	GAG	AAA	AAG	ATA	AAG	AAA	GTA	GTG	GAT	GTT	GGG	TGT	GGG	ATT	617
Glu	Glu	Glu	Lys	Lys	Ile	Lys	Lys	Val	Val	Asp	Val	Gly	Cys	Gly	Ile	
440					445					450					455	
GGA	GGA	AGC	TCA	AGA	TAT	CTT	GCC	TCT	AAA	TTT	GGA	GCT	GAA	TGC	ATT	665
Gly	Gly	Ser	Ser	Arg	Tyr	Leu	Ala	Ser	Lys	Phe	Gly	Ala	Glu	Cys	Ile	
				460					465					470		
GGC	ATT	ACT	CTC	AGC	CCT	GTT	CAG	GCC	AAG	AGA	GCC	AAT	GAT	CTC	GCG	713
Gly	Ile	Thr	Leu	Ser	Pro	Val	Gln	Ala	Lys	Arg	Ala	Asn	Asp	Leu	Ala	
			475					480					485			
GCT	GCT	CAA	TCA	CTC	TCT	CAT	AAG	GCT	TCC	TTC	CAA	GTT	GCG	GAT	GCG	761
Ala	Ala	Gln	Ser	Leu	Ser	His	Lys	Ala	Ser	Phe	Gln	Val	Ala	Asp	Ala	
		490					495					500				
TTG	GAT	CAG	CCA	TTC	GAA	GAT	GGA	AAA	TTC	GAT	CTA	GTG	TGG	TCG	ATG	809
Leu	Asp	Gln	Pro	Phe	Glu	Asp	Gly	Lys	Phe	Asp	Leu	Val	Trp	Ser	Met	
	505					510					515					
GAG	AGT	GGT	GAG	CAT	ATG	CCT	GAC	AAG	GCC	AAG	TTT	GTA	AAA	GAG	TTG	857
Glu	Ser	Gly	Glu	His	Met	Pro	Asp	Lys	Ala	Lys	Phe	Val	Lys	Glu	Leu	
520					525					530					535	
GTA	CGT	GTG	GCG	GCT	CCA	GGA	GGT	AGG	ATA	ATA	ATA	GTG	ACA	TGG	TGC	905
Val	Arg	Val	Ala		Pro	Gly	Gly	Arg	Ile	Ile	Ile	Val	Thr	Trp	Cys	
				540					545					550		
CAT	AGA	AAT	CTA	TCT	GCG	GGG	GAG	GAA	GCT	TTG	CAG	CCG	TGG	GAG	CAA	953
His	Arg	Asn	Leu	Ser	Ala	Gly	Glu	Glu	Ala	Leu	Gln	Pro	Trp	Glu	Gln	
			555					560					565			
AAC	ATC	TTG	GAC	AAA	ATC	TGT	AAG	ACG	TTC	TAT	CTC	CCG	GCT	TGG	TGC	1001
Asn	Ile	Leu	Asp	Lys	Ile	Cys	Lys	Thr	Phe	Tyr	Leu	Pro	Ala	Trp	Cys	
		570					575					580				
TCC	ACC	GAT	GAT	TAT	GTC	AAC	TTG	CTT	CAA	TCC	CAT	TCT	CTC	CAG	GAT	1049
Ser	Thr	Asp	Asp	Tyr	Val	Asn	Leu	Leu	Gln	Ser	His	Ser	Leu	Gln	Asp	
	585					590					595					
ATT	AAG	TGT	GCG	GAT	TGG	TCA	GAG	AAC	GTA	GCT	CCT	TTC	TGG	CCT	GCG	1097
Ile	Lys	Cys	Ala	Asp	Trp	Ser	Glu	Asn	Val	Ala	Pro	Phe	Trp	Pro	Ala	
600					605					610					615	
GTT	ATA	CGG	ACT	GCA	TTA	ACA	TGG	AAG	GGC	CTT	GTG	TCT	CTG	CTT	CGT	1145
Val	Ile	Arg	Thr	Ala	Leu	Thr	Trp	Lys	Gly	Leu	Val	Ser	Leu	Leu	Arg	
				620					625					630		

AGT GGT ATG AAA AGT ATT AAA GGA GCA TTG ACA ATG CCA TTG ATG ATT Ser Gly Met Lys Ser Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile 635 640 645	1193
GAA GGT TAC AAG AAA GGT GTC ATT AAG TTT GGT ATC ATC ACT TGC CAG Glu Gly Tyr Lys Lys Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln 650 655 660	1241
AAG CCA CTC TAA GTCTAAAGCT ATACTAGGAG ATTCAATAAG ACTATAAGAG Lys Pro Leu * 665	1293
TAGTGTCTCA TGTGAAAGCA TGAAATTCCT TAAAAACGTC AATGTTAAGC CTATGCTTCG	1353
TTATTTGTTT TAGATAAGTA TCATTTCACT CTTGTCTAAG GTAGTTTCTA TAAACAATAA	1413
ATACCATGAA TTAGCTCATG TTATCTGGTA AATTCTCGGA AGTGATTGTC ATGGATTAAC	1473
TCAAAAAAAAA AAAAAAAAAA AGGGCGGCCG CTCTAGAGGA TCCAAGCTTA CGTACGCGTG CATGCGACGT CATAAGTCTA TCATACCGTC GACCTCGAGG GGGGCCCTAA ATTCAATTCA	1533 1593
CTGGCCGTCG TTTTACAACG TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCGC	1653
CTTGACGACAC ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC	1713
CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGGACG CGCCCTGTAG CGGCGCATTA	1773
AGCGCGGCGG GTGTGGT	1790

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Ala Thr Leu Ala Ala Pro Ser Ser Leu Thr Ser Leu Pro Tyr 1 5 10 15
Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe Arg Ser 20 25 30
Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val 35 40 45
Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile 50 55 60
Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly 65 70 75 80
Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu 85 90 95
Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser 100 105 110

Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
 115 120 125
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
 130 135 140
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
 145 150 155 160
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
 165 170 175
 Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
 180 185 190
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
 195 200 205
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
 210 215 220
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
 225 230 235 240
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
 245 250 255
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
 260 265 270
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
 275 280 285
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
 290 295 300
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
 305 310 315 320
 Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
 325 330 335
 Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu *
 340 345

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACGGATCCAA AAATGCCTAT GGTTCATCAT CGGGG

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGATCCTG TGGACTTCAA ACTAAAGGCT TTATC

35

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTCATGATT TACCATGTTA GGCC

24

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGATCTCAAA CTAAAGGCTT TATC

24

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCATGCTGTG GCGGCTGCTG CTAC

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACGCAT GCACGCGTAC GTAA

24

QBMAD\162725